Amendment to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

Claims 1-17 (canceled)

Claim 18 (previously presented): A method for detecting a polymorphism in a target nucleic acid sequence, comprising:

receiving hybridization intensities for a first group of probes that are complementary to said target nucleic acid sequence except that the group of probes includes all possible monosubstitutions of positions in said sequence that are within n bases of a base in said sequence that is complementary to said polymorphism, wherein n is from 0 to 5;

receiving hybridization intensities for a second and third group of probes complementary to marker-specific regions upstream and downstream of the polymorphism in the target nucleic acid sequence, wherein the third group of probes differs from the second set of probes at single bases corresponding to known mismatch positions; and

identifying the polymorphism by analyzing the hybridization intensities.

Claim 19 (previously presented): The method of claim 18, wherein the identifying the polymorphism comprises utilizing Principal Component Analysis.

Claim 20 (previously presented): The method of claim 18, wherein at least two alleles of the polymorphism are known.

Claim 21 (previously presented): The method of claim 18, wherein said first groups of probes comprises a plurality of different probes that are complementary to overlapping portions of said target nucleic acid sequence.

Claim 22 (previously presented): The method of claim 18, wherein the monosubstitutions occur at a plurality of distances from a 3' end of said probes.

Claim 23 (previously presented): An method for detecting a polymorphism in a target nucleic acid sequence, said array comprising:

receiving hybridization intensities for a first group of probes that are complementary to said target nucleic acid sequence except that the group of probes includes all

possible monosubstitutions of positions in said sequence that are within n bases of a base in said sequence that is complementary to said polymorphism;

receiving hybridization intensities for a second and third group of probes complementary to marker-specific regions upstream and downstream of the polymorphism in the target nucleic acid sequence, wherein the third group of probes differs from the second set of probes at single bases corresponding to known mismatch positions; and

identifying the polymorphism by analyzing the hybridization intensities.

Claim 24 (previously presented): The method of claim 23, wherein the identifying the polymorphism comprises utilizing Principal Component Analysis.

Claim 25 (previously presented): The method of claim 23, wherein at least two alleles of the polymorphism are known.

Claim 26 (previously presented): The method of claim 23, wherein said first groups of probes comprises a plurality of different probes that are complementary to overlapping portions of said target nucleic acid sequence.

Claim 27 (previously presented): The method of claim 23, wherein the monosubstitutions occur at a plurality of distances from a 3' end of said probes.